6696557

```
  1  GNTCTAGAANTA  GTGGATCCCCCC  GGGCTGCAGGAA  TTCCGACGGCCC  CTGGAAGGGCTC  TGGTGGGGCTGA
     CNAGATCTTNAT  CACCTAGGGGGG  CCCGACGTCCTT  AAGGCTGCCGAG  GACCTTCCCGAG  ACCACCCCGACT

 73  GCGCTCTGCCGC  GGGGGCGCGGGC  ACAGCAGGAAGC  AGGTCCGCGTGG  GGCGCTGGGGGCA TCAGCTACCGGG
     CGCGAGACGGGCG CCCCGCGCCCG   TGTCGTCCTTCG  TCCAGGCGCACC  CGCAGCCGCCGT  AGTCGATGGCCC

145  GTGGTCCGGGCT  GAAGAGCCAGGC  AGCCAAGGCAGC  CACCCGGGGGG   TGGGGACTTTG   GGGGAGTTGGTG
     CACCAGGCCCGA  CTTCTCGGTCCG  TCGGTTCCGTCG  GTGGGCCCCCC   ACCCGCTGAAAC  CCCCTCAACCAC

217  CCCCGCCCCCA   GGCCTTGGCGGG  GTCATGGGGCCC  CCCCATTCTGGG  CCGGGGGGCGTG  CCGAGTCGGGGCC
     GGGGCGGGGGT   CCGGAACCGCCC  CAGTACCCCGGG  GGGTAAGACCC   GGCCCCCGCCAC  GCTCAGCCCGGG
  1                             MetGlyPro     ProHisSerGly  ProGlyGlyVal  ArgValGlyAla

289  CTGCTGCTGCTG  GGGGTTTGGGG   CTGGTGTCTGGG  CTCAGCCTGGAG  AACTCGGCGAAT
     GACGACGACGAC  CCCAAAACCCC   GACCACAGACCC  GAGTCGGACCTC  TTGAGCCGCTTA
 16  LeuLeuLeuLeu  GlyValLeuGly  LeuValSerGly  LeuSerLeuGlu  ProValTyrTrp  AsnSerAlaAsn

361  AAGAGGTTCCAG  GCAGAGGGTGGT  TATGTGCTGTAC  CCTCAGATCGGG  GACCGGCTAGAC  CTGCTCTCTGCCC
     TTCTCCAAGGTC  CGTCTCCCACCA  ATACACGACATG  GGAGTCGTAGCCC CTGGCCGATCTG  GACGAGAGGGG
 40  LysArgPheGln  AlaGluGlyGly  TyrValLeuTyr  ProGlnIleGly  AspArgLeuAsp  LeuLeuCysPro

433  CGGGGCCCGGCT  CCTGCCCCTCAC  TCCTCTCCTAAT  TATGAGTTCTAC  AAGCTGTACCTG  GTAGGGGGTGCT
     GCCCCGGGCCGA  GGACGGGGAGTG  AGGAGAGGATTA  ATACTCAAGATG  TTCGACATGGAC  CATCCCCCACGA
 64  ArgAlaArgPro  ProGlyProHis  SerSerProAsn  TryGluPheTyr  LysLeuTyrLeu  ValGlyGlyAla

505  CAGGGCCGGCGC  TGTGAGGCACCC  CCTGCCCCAAAC  CTCCTTCTCACT  TGTGATCGCCCA  GACCTGGATCTC
     GTCCCGGCGGCCG ACACTCCGTGGG  GGACGGGGTTTG  GAGGAAGAGTGA  ACACTAGCGGGT  CTGGACCTAGAG
 88  GlnGlyArgArg  CysGluAlaPro  ProAlaProAsn  LeuLeuLeuThr  CysAspArgPro  AspLeuAspLeu

577  CGCTTCACCATC  AAGTTCCAGGAG  TATAGCCCTAAT  CTCTGGGGCCAC  GAGTTCCGCTCG  CACCACGATTAC
     GCGAAGTGGTAG  TTCAAGGTCCTC  ATATCGGGATTA  GAGACCCCGGTG  CTCAAGGCGAGC  GTGGTGCTAATG
112  ArgPheThrIle  LysPheGlnGlu  TyrSerProAsn  LeuTrpGlyHis  GluPheArgSer  HisHisAspTyr
```

FIG. 1A

```
649   TACATCATTGCC  ACATCGGATGGG  ACCCGGGAGGGC  CTGGAGAGCCTG  CAGGGAGGTGTG  TGCCTAACCAGA
      ATGTAGTAACGG  TGTAGCCTACCC  TGGGCCCTCCCG  GACCTCTCGGAC  GTCCCTCCACAC  ACGGATTGGTCT
136   TyrIleIleAla  ThrSerAspGly  ThrArgGluGly  LeuGluSerLeu  GlnGlyGlyVal  CysLeuThrArg

721   GGCATGAAGGTG  CTTCTCCGAGTG  GGACAAAGTCCC  CGAGGAGGGCT   GTCCCCCGAAAA  CCTGTGTCTGAA
      CCGTACTTCCAC  GAAGAGGCTCAC  CCTGTTTCAGGG  GCTCCTCCCGA   CAGGGGCTTTT   GGACACAGACTT
160   GlyMetLysVal  LeuLeuArgVal  GlyGlnSerPro  ArgGlyGlyAla  ValProArgLys  ProValSerGlu

793   ATGCCCATGGAA  AGAGACCGAGGG  GCAGCCCACAGC  CTGGAGCCTGGG  AAGGAGAACCTG  CCAGGTGACCCC
      TACGGGTACCTT  TCTCTGGCTCCC  CGTCGGGTGTCG  GACCTCGGACCC  TTCCTCTTGGAC  GGTCCACTGGGG
184   MetProMetGlu  ArgAspArgGly  AlaAlaHisSer  LeuGluProGly  LysGluAsnLeu  ProGlyAspPro

865   ACCAGCAATGCA  ACCTCCCGGGGT  GCTGAAGGCCCC  CTGCCCCCTCCC  AGCATGCCTGCA  GTGGCTGGGGCA
      TGGTCGTTACGT  TGGAGGGCCCCA  CGACTTCCGGGG  GACGGGGGAGGG  TCGTACGGACGT  CACCGACCCCGT
208   ThrSerAsnAla  ThrSerArgGly  AlaGluGlyPro  LeuProProPro  SerMetProAla  ValAlaGlyAla

937   GCAGGGGGGCTG  GCGCTGCTCTTG  CTGGGCGTGGCA  GGGGCTGGGGGT  GCCATGTGTTGG  CGGAGACGGCGG
      CGTCCCCCCGAC  CGCGACGAGAAC  GACCCGCACCGT  CCCCGACCCCCA  CGGTACACAACC  GCCTCTGCCGCC
232   AlaGlyGlyLeu  AlaLeuLeuLeu  LeuGlyValAla  GlyAlaGlyGly  AlaMetCysTrp  ArgArgArgArg

1009  GCCAAGCCTTCG  GAGAGTCGCCAC  CCTGTCCTGGC   TCCTTCGGGAGG  GGAGGGTCTCTG  GGCCTGGGGGGT
      CGGTTCGGAAGC  CTCTCAGCGGTG  GGACCAGGACCG  AGGAAGCCCTCC  CCTCCCAGAGAC  CCGGACCCCCCA
256   AlaLysProSer  GluSerArgHis  ProGlyProGly  SerPheGlyArg  GlyGlySerLeu  GlyLeuGlyGly

1081  GGAGGTGGGATG  GGACCTCGGGAG  GCTGAGCCTGGG  GAGCTAGGGATA  GCTCTCGCGGGT  GGCGGGGGCTGCA
      CCTCCACCCTAC  CCTGGAGCCCTC  CGACTCGGACCC  CTCGATCCCTAT  CGAGAGCGCCCA  CCGCCCCCGACGT
280   GlyGlyGlyMet  GlyProArgGlu  AlaGluProGly  GluLeuGlyIle  AlaLeuArgGly  GlyGlyAlaAla

1153  GATCCCCCCTTC  TGCCCCCACTAT  GAGAAGGTGAGT  GGTGACTATGGG  CATCCTGTGTAT  ATCGTGCAGGAT
      CTAGGGGGGAAG  ACGGGGGTGATA  CTCTTCCACTCA  CCACTGATACCC  GTAGGACACATA  TAGCACGTCCTA
304   AspProProPhe  CysProHisTyr  GluLysValSer  GlyAspTyrGly  HisProValTyr  IleValGlnAsp

1225  GGGCCCCCCCAG  AGCCCTCCAAAC  ATCTACTACACA  TCGATTTCTGTG  TTGGAGTGGCCC  ATATTGCATACG
      CCCGGGGGGGTC  TCGGGAGGTTTG  TAGATGATGTGT  AGCTAAAGACAC  AACCTCACCGGG  TATAACGTATGC
328   GlyProProGln  SerProProAsn  IleTyrTyrThr  SerIleSerVal  LeuGluTrpPro  IleLeuHisThr
```
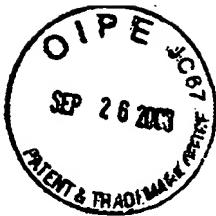
FIG. 1B

```
1297  ATACAACTGTTT  TTCATGCGATCC  AAGTGCTCCCGT  GTCACTACACATTC  TTATTCCTGTG  CAAGTTATTACG
      TATGTTGACAAA  AAGTACGCTAGG  TTCACGAGGGCA  CAGTGATGTAAG  AATAAAGGACAC  GTTCAATAATGC
352   IleGlnLeuPhe  PheMetArgSer  LysCysSerArg  ValThrThrThrPhe  LeuPheProVal  GlnValIleThr

1369  ACATCGACTTGC  CGGATGACTTCA  TTTAGCTTTACC  ACCCTGAACCCA  TCCATGCAGGCC  TGCAGAGCACAG
      TGTAGCTGAACG  GCCTACTGAAGT  AAATCGAAATGG  TGGGACTTGGGT  AGGTACGTCCGG  ACGTCTCGTGTC
376   ThrSerThyCys  ArgMetThrSer  PheSerPheThr  ThrLeuAsnPro  SerMetGlnAla  CysArgAlaGln

1441  ATGGGGGAATTC  CGAATCAGATGG  TGTTTCTGGGGG  GACAGGATCCTG  GGTACGGCTCTG  TTTGTGCTTGTG
      TACCCCCTTAAG  GCTTAGTCTACC  ACAAAGACCCCC  CTGTCCTAGGAC  CCATGCCGAGAC  AAACACGAACAC
400   MetGlyGluPhe  ArgIleArgTrp  CysPheTrpGly  AspArgIleLeu  GlyThrAlaLeu  PheValLeuVal

1513  CTTATTCTTCTT  CTTGGGAGGCTG  AATATGCATCAG  ACGACACTGCTC  CGGCAACGGGCC  AGTGTGGAGGCG
      GAATAAGAAGAA  GAACCCTCCGAC  TTATACGTAGTC  TGCTGTGACGAG  GCCGTTGCCCGG  TCACACCTCCGC
424   LeuIleLeuLeu  LeuGlyArgLeu  AsnMetHisGln  ThrThrLeuLeu  ArgGlnArgAla  SerValGluAla

1585  GAAGCCGGCCAG  CATGGTCCCCTG  TGATAGGATTGA  AAGAGCTACTGA  GAATAGGGGGCT  TCTCAATGAGAG
      CTTCGGCCGGTC  GTACCAGGGGAC  ACTACTCCTAACT  TTCTCGATGACT  CTTATCCCCCGA  AGAGTACTCTC
448   GluAlaGlyGln  HisGlyProLeu  (SEQ ID NO: 2)

1657  AGCGGAGGCTGC  TGTTATCATGGG  AACCAGGCAGAT  CAATCATCCCTG  GCAGGTCAGGCA  GGAAGTTACTTA
      TCGCCTCCGACG  ACAATAGTACCC  TTGGTCCGTCTA  GTTAGTAGGGAC  CGTCCAGTCCGT  CCTTCAATGAAT

1729  GCTTCTCCTTCA  CCTTCTTCCCAC  AGAATTTATTAT  AGGCTTGTTCCA  AGTTGTAGTGTG  TGATCAGATTCG
      CGAAGAGGAAGT  GGAAGAAGGGTG  TCTTAAATAATA  TCCGAACAAGGT  TCAACATCACAC  ACTAGTCTAAGC

1801  TGCTGCCTGTCA  GCTCTGTGCTAC  CTGGCAGTTCCC  CTCATGGAATTC  GATATCAAGCTT  ATCGGATACCGTC
      ACGACGGACAGT  CGAGACACGATG  GACCGTCAAGGG  GAGTACCTTAAG  CTATAGTTCGAA  TAGCTATGGCAG

1873  GACCT  (SEQ ID NO: 1)
      CTGGA
```

FIG. 1C

FIG. 1A
FIG. 1B
FIG. 1C

FIG. 1

```
1    GNTCTAGAANTA GTGGATCCCCCC GGGCTGCAGGAA TTCCGACGGCCC TGGTGGGGCTGA
     CNAGATCTTNAT CACCTAGGGGGG CCCGACGTCCTT AAGGCTGCCGGG ACCACCCCGACT

73   GCGCTCTGCCGC GGGGGCGGGGGC ACAGCAGGAAGC AGGTCCGCGTGG GCGCTGGGGGCA TCAGCTACCGGG
     CGCGAGACGGCG CCCCCGCCGCCCG TGTCGTCCTTCG TCCAGGCGCACC CGCGACCCCGT AGTCGATGGCCC

145  GTGGTCCGGGCT GAAGAGCCAGGC AGCCAGGCAGC CACCCCGGGGGG TGGGCGGACTTTG GGGGGAGTTGGTG
     CACCAGGCCCGA CTTCTCGGTCCG TCGGTTCCGTCG GTGGGCCCCCC ACCCGCTGAAAC CCCCTCAACCAC

217  CCCCGCCCCCCA GGCCTTGGCGGG GTCATGGGGCCC CCCATTCTGGG CGAGTCGGGGCC
     GGGGCGGGGGGT CCGGAACCGCCC CAGTACCCCGGG GGGGTAAGACCC GCTCAGCCCCGG
1                             MetGlyPro    ProHisSerGly ProGlyGlyVal ArgValGlyAla

289  CTGCTGCTGCTG GGGGTTTTGGGG CTGGTGTCTGGG CTCAGCCTGGAG AACTCGGCGAAT
     GACGACGACGAC CCCCAAAACCCC GACCACAGACCC GAGTCGGACCTC TTGAGCCGCTTA
16   LeuLeuLeuLeu GlyValLeuGly LeuSerLeuGly ProValTyrTrp AsnSerAlaAsn

361  AAGAGGTTCCAG GCAGAGGGTGGT TATGTGCTGTAC CCTCAGATCGGG GACCGGCTAGAC
     TTCTCCAAGGTC CGTCTCCCACCA ATACACGACATG GGAGTCTAGCCC CTGGCCGATCTG
40   LysArgPheGln AlaGluGlyGly TyrValLeuTyr ProGlnIleGly AspArgLeuAsp

433  CGGGCCCGGCCT CCTGGCCCCTCAC TCCTCTCCTAAT TATGAGTTCTAC AAGTCTGTACCTG GTAGGGGGTGCT
     GCCCGGGCCGGA GGACCGGGGAGTG AGGAGAGGATTA ATACTCAAGATG TTCGACATGGAC CATCCCCCACGA
64   ArgAlaArgPro ProGlyProHis SerSerProAsn TrpGluPheTyr LysLeuTyrLeu ValGlyGlyAla

505  CAGGGCCGGCGC TGTGAGGCACCC CCTGCCCCAAAC CTCCTTCTCACT TGTGATCGGCCA GACCTGGATCTC
     GTCCCGGCCGCG ACACTCCGTGGG GGACGGGGTTTG GAGGAAGAGTGA ACACTAGCCGGT CTGGACCTAGAG
88   GlnGlyArgArg CysGluAlaPro ProAlaProAsn LeuLeuLeuThr CysAspArgPro AspLeuAspLeu

577  CGCTTCACCATC AAGTTCCAGGAG TATAGCCCTAAT CTCTGGGGCCAC GAGTTCCGGCTCG CACCACGATTAC
     GCGAAGTGGTAG TTCAAGGTCCTC ATATCGGGATTA GAGACCCCGGTG CTCAAGGCCGAGC GTGGTGCTAATG
112  ArgPheThrIle LysPheGlnGlu TyrSerProAsn LeuTrpGlyHis GluPheArgSer HisHisAspTyr
```

FIG. 2A

```
649   TACATCATTGCC  ACATGGGATGGG  ACCGGGGAGGGC  CTGGAGAGCCTG  CAGGGAGGTGTG  TGCCTAACCAGA
      ATGTAGTAACGG  TGTAGCCTACCC  TGGGCCCTCCCG  GACCTCTCGGAC  GTCCCTCCACAC  ACGGATTGGTCT
136   TyrIleIleAla  ThrSerAspGly  ThrArgGluGly  LeuGluSerLeu  GlnGlyGlyVal  CysLeuThrArg

721   GGCATGAAGGTG  CTTCTCCGAGTG  GGACAAAGTCCC  CGAGGAGGGGCT  GTCCCCCGAAAA  CCTGTGTCTGAA
      CCGTACTTCCAC  GAAGAGGCTCAC  CCTGTTTCAGGG  GCTCCTCCCCGA  CAGGGGGCTTTT  GGACACAGACTT
160   GlyMetLysVal  LeuLeuArgVal  GlyGlnSerPro  ArgGlyGlyAla  ValProArgLys  ProValSerGlu

793   ATGCCCATGGAA  AGAGACCGAGGG  GCAGCCCACAGC  CTGGAGCCTGGG  AAGGAGAACCTG  CCAGGTGACCCC
      TACGGGTACCTT  TCTCTGGCTCCC  CGTCGGGTGTCG  GACCTCGGACCC  TTCCTCTTGGAC  GGTCCACTGGGG
184   MetProMetGlu  ArgAspArgGly  AlaAlaHisSer  LeuGluProGly  LysGluAsnLeu  ProGlyAspPro

865   ACCAGCAATGCA  ACCTCCCGGGGT  GCTGAAGGCCCC  CTGCCCCCTCCC  AGCATGCCTGCA  GTGGCTGGGGCA
      TGGTCGTTACGT  TGGAGGGCCCCA  CGACTTCCGGGG  GACGGGGGAGGG  TCGTACGGACGT  CACCGACCCCGT
208   ThrSerAsnAla  ThrSerArgGly  AlaGluGlyPro  LeuProProPro  SerMetProAla  ValAlaGlyAla

937   GCAGGGGGGCTG  CTGGGCGTGGCA  CTGGGGCGTGGCA  GGGGCTGGGGGT  GCCATGTGTTGG  CGGAGACGGCGG
      CGTCCCCCCGAC  GACCCGCACCGT  CCCCGACCCCCA  CCCCGACCCCCA  GGTACACAACC  GCCTCTGCCGCC
232   AlaGlyGlyLeu  AlaLeuLeuLeu  LeuGlyValAla  GlyAlaGlyGly  AlaMetCysTrp  ArgArgArgArg

1009  GCCAAGCCTTCG  GAGAGTCGCCAC  CCTGGTCCTGGC  TCCTTCGGGAGG  GGAGGGTCTCTG  GGCCTGGGGGGT
      CGGTTCGGAAGC  CTCTCAGCGGTG  GGACCAGGACCG  AGGAAGCCCTCC  CCTCCCAGAGAC  CCGGACCCCCCA
256   AlaLysProSer  GluSerArgHis  ProGlyProGly  SerPheGlyArg  GlyGlySerLeu  GlyLeuGlyGly

1081  GGAGGTGGGATG  GGACCTCGGGAG  GCTGAGCCTGGG  GAGCTAGGGATA  GCTCTGCGGGGT  GGCGGGGCTGCA
      CCTCCACCCTAC  CCTGGAGCCCTC  CGACTCGGACCC  CTCGATCCCTAT  CGAGACGCCCCA  CCGCCCCGACGT
280   GlyGlyGlyMet  GlyProArgGlu  AlaGluProGly  GluLeuGlyIle  AlaLeuArgGly  GlyGlyAlaAla

1153  GATCCCCCCTTC  TGCCCCCACTAT  GAGAAGGTGAGT  GGTGACTATGGG  CATCCTGTGTAT  ATCGTGCAGGAT
      CTAGGGGGGAAG  ACGGGGGTGATA  CTCTTCCACTCA  CCACTGATACCC  GTAGGACACATA  TAGCACGTCCTA
304   AspProProPhe  CysProHisTyr  GluLysValSer  GlyAspTyrGly  HisProValTyr  IleValGlnAsp

1225  GGGCCCCCCCAG  AGCCCTCCAAAC  ATCTACTACAAG  GTATGAGGGGCTC  TTGGAGTGGCCC  ATATTGCATACG
      CCCGGGGGGGTC  TCGGGAGGTTTG  TAGATGATGTTC  CATACTCCCGAG  AACCTCACCGGG  TATAACGTATGC
328   GlyProProGln  SerProProAsn  IleTyrTyrLys  ValOP*  (SEQ ID NO: 4)
```

FIG. 2B

1297 AGCCCTTCTTGG GGTGCTCCTCCA GTTTAATTCCTG GTTTGAGGGACA CCTCTAACATCT CGGCCCCCTGTG
      TCGGGAAGAACC CCACGGAGGAGGT CAAATTAAGGAC CAAACTCCCTGT GGAGATTGTAGA GCCGGGGGACAC

1369 CCCCCCAGCCC CTTCACTCCTCC CGGCTGCTGTCC TCGTCTCCACTT TTAGGATTCCTT AGGATTCCCACT
      GGGGGGTCGGG GAAGTGAGGAGG GCCGACGACAGG AGCAGAGGTGAA AATCCTAAGGAA TCCTAAGGGTGA

1441 GCCCCACTTCCT GCCCTCCCGTT GGCCATGGGTGC CCCCCTCCTGTCT CAGTGTCCCTGG ATCCTTTTTCCT
      CGGGGTGAAGGA CGGGAGGGCAAA CCGGTACCCACG GGGGGAGACAGA GTCACAGGGACC TAGGAAAAGGA

1513 TGGGGAGGGGCA CAGGCTCAGCCT CCTCTCTGACCA TGACCCAGGCAT CCTTGTCCCCCT CACCCACCCAGA
      ACCCCTCCCCGT GTCCGAGTCGGA GGAGAGACTGGT ACTGGGTCCGTA GGAACAGGGGGA GTGGGTGGGTCT

1585 GCTAGGGGCGGG AACAGCCCACCT TTTGGTTGGCAC CGCCTTCTTTCT GCCTCTCACTGG TTTTCTCTTCTC
      CGATCCCCGCCC TTGTCGGGTGGA AAACCAACCGTG GCGGAAGAAAGA CGGAGAGTGACC AAAGAGAAGAG

1657 TATCTCTTATTC TTTCCCTCTCTT CCGTCTCTAGGT CTGTTCTTCTTC CTAGCATCCTC CTCCCCACATCT
      ATAGAGAATAAG AAAGGGAGAGAA GGCAGAGATCCA GACAAGAAGAAG GGATCGTAGGAG GAGGGGTGTAGA

1729 CCTTCACCCTC TTGGCTTCTTAT CCTGTGCCTCTC CCATCTCCTGGG TGGGGGCATCAA AGCATTCTCCC
      GGAAAGTGGGAG AACCGAAGAATA GGACACGGAGAG GGTAGAGGACCC ACCCCGTAGTT TCGTAAAGAGGG

1801 CTTAGCTTTCAG CCCCCCTTCTGA CCTCTCATACCA ACCACTCCCCTC AGTCTGCCAAAA ATGGGGGCCTTA
      GAATCGAAAGTC GGGGGGAAGACT GGAGAGTATGGT TGGTGAGGGGAG TCAGACGGTTTT TACCCCCGGAAT

1873 TGGGGAAGGCTC TGACACTCCACC CCAGCTCAGGCC ATGGGCACCAGG GCTCCATTCTCT GGCCTGGCCCAG
      ACCCCTTCCGAG ACTGTGAGGTGG GGTCGAGTCCGG TACCCGTCGTCC CGAGGTAAGAGA CCGGACCGGGTC

1945 GCCTCTACATAC TTACTCCAGCCA GGGTCATGACAG CTACCATGAGAA GGGTCATGACAG GAAGTGTCCCGT
      CGGAGATGTATG AATGAGGTCGGT AAACCCCACCAA CCCAGTACTGTC GATGGTACTCTT CTTCACAGGGCA

2017 TTTGTCCSGTGG CCAATAGCAAGA TATGAACCGGTC GGGACATGTATG TGCTGAATGGGC
      AAACAGGTCACC GGTTATCGTTCT ATACTTGGCCAG CCCTGTACATAC CTGAACCAGACT ACGACTTACCCG

FIG. 2C

```
2089  CACTTGGGGACCG  GAAGTGACTTGC  TCCAGACAAGAG  GTGACCAGCCCC  GGACAGAAATGG  CCTGGGAAGTAG
      GTGAACCCTGGC  CTTCACTGAACG  AGGTCTGTTCTC  CACTGGTCCGGG  CCTGTCTTTACC  GGACCCTTCATC

2161  CAGAAGCAGTGC  AGCAGGAACTGG  AAGTGCCTTCAT  CCAGGACAGGAA  GTAGCACTTCTG  AAACAGGAAGTG
      GTCTTCGTCACG  TCGTCCTTGACC  TTCACGGAAGTA  GGTCCTGTCCTT  CATCGTGAAGAC  TTTGTCCTTCAC

2233  GTCTGGCTGGAA  CTCCAAGTGGCT  TAGTCTGGGGGA  TCAGGAGGTGGG  AGGTGGATGGTT  CTTATTCTGTGG
      CAGACCGACCTT  GAGGTTCACCGA  ATCAGACCCCCT  AGTCCTCCACCC  TCCACCTACCAA  GAATAAGACACC

2305  AGAAGAAGGGCG  GGAAGAACTTCC  TTTCAGGAGGAA  GCTGGAACTTAC  TGACTGTAAGAG  GTTAGAGGTGGA
      TCTTCTTCCCGC  CCTTCTTGAAGG  AAAGTCCTCCTT  CGACCTTGAATG  ACTGACATTCTC  CAATCTCCCACCT

2377  CCGA (SEQ ID NO: 3)
      GGCT
```

FIG. 2D

| FIG. 2A |
| FIG. 2B |
| FIG. 2C |
| FIG. 2D |

FIG. 2

```
AL-2b.L    1  GNTCTAGAANTAGTGGATCCCCCGGGCTGCAGGAATTCCGACGGCCCCT
AL-2b.L   51  GGAAGGGCTCTGGTGGGGCTGAGCGGCTCTGCCGCGGGGGCGCGGGCACAG
AL-2b.L  101  CAGGAAGCAGGTCCGCGCCGCTGGGGGGCCATCAGCTACCGGGGGTGGTC
AL-2b.L  151  CGGGCTGAAGAGCCAGGCAGCCAAGGCCCCCCGGGGGGTGGGGCGAC
AL-2b.L  201  TTTGGGGGAGTTGGTGCCCGCCCAGGCCTTGGCGGGGTCATGGGGC
AL-2b.L  251  CCCCCATTCTGGGCGGGGGGGGTGCGGTCGGGGCCCTGCTGCTG
AL-2b.L  301  GGGTTTTGGGGCTGGTGTCTGGGCTCTGGAGCCTGTCTCTACTGGAA
AL-2b.L  351  CTCGGCGAATAAGAGGTTCCAGGCAGAGGGTGGTTATGTGCTGTACCCTC
AL-2b.L  401  AGATCGGGGACCGGCTAGACCTGCTCTGCCCCCGGCCCTCCTGGC
AL-2b.L  451  CCTCACTCCTCCTCCTAATTATGAGTTCTACAAGCTGTACCTGGTAGGGGG

AL-2b.L  501  TGCTCAGG GCCG GCGCTGTGAGGCACCCCCTGCCCCAAACCTCCTTCTCA
H10006     1       ------ GCCGA CGCTGTGAGGCACCCCCTGCCCCAAACCTCCTCCTCA
AL-2b.L  551  CTTGTGATCGCCCAGACCTGGATCTCGGCCTTCACCATCAAGTTCCAGGAG
H10006    43  CTTGTGATCGCCCAGACCTGGATCTCGGCCTTCACCATCAAGTTCCAGGAG
AL-2b.L  601  TATAGCCCTAATTCTCTGGGCCACGAGTTCCGCGCCACGATTACTA
H10006    93  TATAGCCCTAATTCTCTGGGCCACGAGTTCCGCGCCACCACGATTACTA
AL-2b.L  651  CATCATTGCCACATCGGGATGGGACCCCGGGAGG GC CTGGAGAGCCTGCAGG
H10006   143  CATCATTGCCACATCGGGATGGGACCCCGGGAGG CT GGGAGAGCCTGCAGG
AL-2b.L  701  GA GTGTGTGCCTAACCAGAGGCATGAAGGTGCTTCTCCGAGTG GGGACAA
H10006   193  GA AGTGTGTGCCTAACCAGAGGCATGAAGGTGCTTCTCCGAGTG NGGACAA
```

FIG. 3A

```
AL-2b.L  751  AGT CCCCGAGGAGGGGCTGTCCCCGAAAACCTGTGTCTGAAATGCCCAT
H10006   243  AGT -CCCGAGGAGGGGCTGTCCCCGAAAACCTGTGTCTGAAATGCCCAT

AL-2b.L  801  GGAAAGAGACCGAGGGGCAGCCCACCAGCCT-GGGAAGGAGAA
H10006   292  GGAAAGAGACCGAGGGGCAGCCCACCAGCCTGGGGAAGGAGAA

AL-2b.L  849  CCTGCCCAGGTGACCCCACCAGCAATGCAACCTCCCGGGGT--GCTGAAGG
H10006   342  CCTGCCCAGGTGACCCCACCAGCAATNCAACCTTCCGGGGTTGCTTGAAGG

AL-2b.L  897  CCCCCT--GCCCTCCCAGCA-TGCCTGCAGT-GGCTGGGGGCAGCAGG
H10006   392  GCCCCTTGACCCTTTCCCAGCATTGCNTGCANTTGGTTNGGGGCAGCANG

AL-2b.L  942  GGGGC----TGGCGCTGCTCTTGCTGGGCGTGGCAGGGGCTGGGGGGTGCC
H10006   442  GGGGNGTTTTTGGC (SEQ ID NO: 5)

AL-2b.L  988  ATGTGTTGGCGGAGACGGCGGGGCCAAGCCTTCGGAGAGTCGCCACCCTGG

AL-2b.L 1038  TCCTGGCTCCTTCGGGAGGGGAGGGTCTCTGGGCCTGGGGGGGTGGAGGTG

AL-2b.L 1088  GGATGGGACCTCGGGAGGCTGAGCCTGGGGAGCTAGGGATAGCTCTGCGG

AL-2b.L 1138  GGTGGCGGGGGCTGCAGATCCCCCCTTCTGCCCCTTGTGTATATCGTGCGG

AL-2b.L 1188  TGGTGACTATGGGCATCCTCCTGTGTTGTTGGGCCCCCCAGA

AL-2b.L 1238  GCCCTCCAAACATCTACTACACATCGATTTCTGTGTTGGGCCCCATA

AL-2b.L 1288  TTGCATACGATACAACTGTTTTCATGCGATCCAAGTGCTCCCGTGTCAC
```

FIG. 3B

AL-2b.L1338 TACATTCTTATTTCCTGTGCAAGTTATTACGACATCGACTTGCCGGATGA

AL-2b.L1388 CTTCATTTAGCTTTACGACCCTGAACCCATCCATGCAGGCCTGCAGAGCA

AL-2b.L1438 CAGATGGGGGAATTCCGAATCAGATGGTGTTTCTGGGGGACAGGATCCT

AL-2b.L1488 GGGTACGGCTCTGTTTGTGCTTTCTTCTTCTTGGGAGGCTGA

AL-2b.L1538 ATATGCATCAGACGACAGTGCTCCGGCAACGGGCCAGTGTGGAGGCGGAA

AL-2b.L1588 GCCGGCCAGCATGGTCCGCTGTGATAGGATTGAAAGAGCTACTGAGAATA

AL-2b.L1638 GGGGGCTTCTCAATGAGAGAGCGGAGGCTGCTGTTATCATGGGAACCAGG

AL-2b.L1688 CAGATCAATCATCCCTGGCAGGTCAGGTACTTAGCTTCTCCT

AL-2b.L1738 TCACCTTCTTCCCACAGAATTTATTATAGGCTTGTTCCAAGTTGTAGTGT

AL-2b.L1788 GTGATCAGATTCGTGCTGCCTGTCAGCTCTGTCTGCTACCTGGCAGTTCCCC

AL-2b.L1838 TCATGGAATTCGATATCAAGCTTATCGATATACCGTCGACCT (SEQ ID NO: 1)

FIG. 3C

| FIG. 3A |
| FIG. 3B |
| FIG. 3C |

FIG. 3

```
lerk2      1  MA-RPGQRWLGKWLVAMVVWALCRLATPLAKNLEPVSWSSLNPKFLSGKG
huHTKL     1  MAVRRDSVWKYCWGVLMV---LCRTAISKSIVLEPIYWNSSNSKFLPGQG
AL2.sht    1  MG-PPHSGPGGVRVGALLLGVLGLVSGL--SLEPVYWNSANKRFQAEGG
AL2.long   1  MG-PPHSGPGGVRVGALLLGVLGLVSGL--SLEPVYWNSANKRFQAEGG

lerk2     50  LVIYPKIGDKLDIICPRA---EAGR--PYEYYKLYLVRPEQAAACSTVLD
huHTKL    48  LVLYPQIGDKLDIICPKV---DSKTVGQYEYYKVYMVDKDQADRCTIKKE
AL2.sht   48  YVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPA
AL2.long  48  YVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPA

lerk2     95  PNVLVTCNRPEQEIRFTIKFQEFSPNYMGLEFKKHHDYYITSTSNGSLEG
huHTKL    95  NTPLLNCAKPDQDIKFTIKFQEFSPNLWGLEFQKNKDYYIISTSNGSLEG
AL2.sht   98  PNLLLTCDRPDLDRFTIKFQEYSPNLWGHEFRSHHDYYIIATSDGTREG
AL2.long  98  PNLLLTCDRPDLDRFTIKFQEYSPNLWGHEFRSHHDYYIIATSDGTREG

lerk2    145  LENREGGVCRTRTMKIIMKVGQDPNAVTPEQLTTSRPSKEADNTVKMATQ
huHTKL   145  LDNQEGGVCQTRAMKILMKVGQDASS-----AGSTRNKDPTRRPELEAG
AL2.sht  148  LESLQGGVCLLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMERDRGAAHSLE
AL2.long 148  LESLQGGVCLLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMERDRGAAHSLE
```

FIG. 4A

```
lerk2    195  APGSRGSLGDSDGKHETVNQEEKSGPGASGGSSGDPDGFFNSKVALFAAV
huHTKL   189  TNG-RSSTTSPFVKPNPGSSTDGNSAGHSG----NNILGSEVALFAGI
AL2.sht  198  -PGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGL---ALLLGVA
AL2.long 198  -PGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGL---ALLLGVA

lerk2    245  GAGCVIFLLIIIFLLTVLLLKLRKRHRKHTQ-QRAAALSLSTLASPKGGSG
huHTKL   232  ASGCIIFIVIIITLVLLKYRRHRKHSP-QHTTTLSLSTLATPKRSGN
AL2.sht  244  GAGGA-----MCWRRRAKPSESRHPGPGSFGRGGSLGLGG----GGGMG
AL2.long 244  GAGGA-----MCWRRRAKPSESRHPGPGSFGRGGSLGLGG----GGGMG

lerk2    294  TAGTEPSDIIIPLR---TENNYCPHYEKVSGDYGHPVYIVQEMPPQSPA
huHTKL   261  NNGSEPSDIIIPLR---TADSVFCPHYEKVSGDYGHPVYIVQEMPPQSPA
AL2.sht  265  PREAEPGELGIALRGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPP
AL2.long 295  PREAEPGELGIALRGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPP

lerk2    341  NIYY-----
huHTKL   328  NIYY-----
AL2.sht  335  NIYY-----
AL2.long 335  NIYYTSISVLEWPILHTIQLFFMRSKCSRVTTFLFPVQVITTSTCRMTSF
```

FIG. 4B

```
lerk2    345 - - - - - - - - - - - - - - - - - - - - - KV - - -   (SEQ ID NO: 9)
huHTKL   332 - - - - - - - - - - - - - - - - - - - - - KV - - -   (SEQ ID NO: 10)
AL2.sht  339 - - - - - - - - - - - - - - - - - - - - - KV - - -   (SEQ ID NO: 4)
AL2.long 385 S F T T L N P S M Q A C R A Q M G E F R I R W C F W G D R I L G T A L F V L V L I L L L G R L N M H

AL2.long 435 Q T T L L R Q R A S V E A E A G Q H G P L   (SEQ ID NO: 2)
```

FIG. 4C

| FIG. 4A |
| FIG. 4B |
| FIG. 4C |

FIG. 4

```
LERK2     1  MA-RPGQRMLSKMLVAMVLTLCRLATPLAKNLEPVSWSSLNPKFLSGKG
huHTKL    1  MAVRRDSVMKYCWGVLMV---LCRTAISKSIVLEPIYWNSSNSKFLPGQG
AL2.long  1  MGPPHSGP-GGVRVGALLL--LGVLGLVSGLSLEPVYWNSANKRFQAEGG

LERK2    50  LVIYPKIGDKLDIICPRA------EAGR--PYEYYKLYLVRPEQAACSTVLD
huHTKL   48  LVLYPQIGDKLDIICPKV------DSKTVGQYEYYKVMVDKDQADRCTIKKE
AL2.long 48  YVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYLVGGAGGRRCEAPPA

LERK2    95  PNVLVTCNKPHQEIRFTIKFQEFSPNYMGLEFKKYHDYIITSNGSLEG
huHTKL   95  NTPLLNCAKPDQDIKFTIKFQEFSPNLWGLEFQKNKDYYIISTNGSLEG
AL2.long 98  PNLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHHDYYIIATSDGTREG

LERK2   145  LENREGGVCRTRTMKIVMKVGQDPNAVTPEQLTTSRPSKESDNTVKTATQ
huHTKL  145  LDNQEGGVCQTRAMKILMKVGQDASS-----AGSTRNKDPTRRPELEAG
AL2.long148  LESLQGGVCLTRGMKVLLRVGQSPRG-----GAVPRKPVSEMPMERDRG

huHTKL  195  APGRGSQGDSDGKHETVNQEEKSGPGAGGGSGDSDSFFNSKVALFAAVG
AL2.sht 189  TNGRSSTTSPFVKPNPGSSTDGNSAGHSG-----NNILGSEVALFAGIIA
AL2.long192  AAHSLEPGKENLPGDPTSNATSRGAE------GPLPPPSMPAVAGAIA
```

FIG. 5A

LERK2   245 AGCVIFLLIIFLTVLLKLRKRHRKHTQQRAAALSL--STLASPKGGS
huHTKL   233 SGCIIFIVIITLVVLLKYRRRHRKHSPQHTTTLSL--STLATPKRSG
AL2.long 233 GGLALLLLGVAGAGGAMCWRRRRAKPSESRHPGPGSFGRGGSLGLGGGGG

LERK2   292 -GTAGTEPSDIIIPLR---TENNYCPHYEKVSGDYGHPVYIVQEMPPQS
huHTKL   280 -NNNGSEPSDIIIPLR---TADSVFCPHYEKVSGDYGHPVYIVQEMPPQS
AL2.long 283 MGPREAEPGELGIALRGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQS

LERK2   338 PANIYY-------------------------------------
huHTKL   326 PANIYY-------------------------------------
AL2.long 333 PPNIYYTSISVLEWPILHTIQLFFMRSKCSRVTTFLFPVQVITTSTCRMT

LERK2   344 ------KV---------------------------------- (SEQ ID NO:9)
huHTKL   332 ------KV---------------------------------- (SEQ ID NO:10)
AL2.long 383 SFSFTTLNPSMQACRAQMGEFRIRWCFWGDRILGTALFVLLILLGRLN

AL2.long 433 MHQTTLLRQRASSVEAEAGQHGPL (SEQ ID NO:2)

FIG. 5B

| FIG. 5A |
| FIG. 5B |

FIG. 5